

Molecular Co-evolution of the Rice *Pi-ta* Resistance Gene and *Magnaporthe Grisea* Avirulence Gene *AVR-Pita*

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Resistance to a biotrophic pathogen is often governed by a gene-for-gene relationship. A resistance (*R*) gene is effective in preventing infection by the pathogen containing the corresponding avirulence (*AVR*) gene. Molecular characterization of over 48 plant *R* genes has advanced the ability to breed for effective resistance against pathogens. Knowledge of DNA sequences of susceptible and resistant alleles not only enhances our understanding of *R* gene evolution, but can also be used to identify nucleotides that distinguish the resistant counterpart. These unique DNA sequences can be used to develop *R* gene specific primers to amplify portions of an *R* gene to use as a marker for marker-assisted selection (MAS). Blast disease is one of the most destructive rice diseases worldwide. The *Pi-ta* resistance gene is one of those *R* genes characterized at the molecular level. *Pi-ta* encodes a putative cytoplasmic protein with nucleotide binding sites and a leucine rich repeat. *AVR-Pita* encodes a metalloprotease, and its processed form AVR-Pita₁₇₆ interacts directly with the *Pi-ta* protein to trigger complete resistance to *Magnaporthe grisea* races containing the corresponding avirulence gene *AVR-Pita*. One resistant *Pi-ta* and three susceptible *pi-ta* alleles were identified from rice germplasm. An alignment of DNA sequences of these *Pi-ta* haplotypes identified several conserved nucleotide substitutions, and these nucleotide differences were used to develop PCR based markers for stacking the *Pi-ta* gene into advanced rice breeding lines by MAS. Similarly, results of structural and functional studies of *avr-pita* alleles in US *M. grisea* pathotypes suggest that transposition, insertion and deletion of DNA sequences at the *AVR-Pita* locus may be responsible for the instability of *AVR-Pita*, and thus it is a likely mechanism to defeat the resistance mediated by *Pi-ta*. Recent progress in understanding the coevolution of a plant *R* gene and a corresponding pathogen *AVR* gene and in developing the molecular methods for rice breeding and crop protection will be presented.